In the Claims:

1. (withdrawn). A retroviral display library, said library comprising a plurality of retroviruses wherein each retrovirus differs in relation to other retroviruses in the plurality as to the amino acid sequence of an Env protein, each member of the plurality comprising nucleic acid that codes for both said Env protein and a cell-selection marker.

2. (withdrawn). A library of Claim 1 wherein the size of the plurality is more than 1 x 10^5.

3. (withdrawn). A library of Claim 1 wherein the Env protein comprises a nonviral cell- binding peptide.

4. (withdrawn). A library of Claim 1 wherein the cell selection marker is a drug resistance marker.

5. (withdrawn). A retroviral Env library, said library comprising a plurality of Env proteins wherein the amino acid sequence of each Env protein differs in relation to the amino acid sequence of the other Env proteins in the plurality.

6. (withdrawn). A library of Claim 5 wherein the size of the plurality is more than 1 x 10^5.

7. (withdrawn). A library of Claim 5 wherein the Env protein comprises a nonviral cell- binding peptide.

8. (withdrawn). A retroviral nucleic acid library said library comprising a plurality of retroviral nucleic acid molecules, each of said molecules coding for a retroviral Env protein

and a cell-selection marker, and wherein each of said nucleic acid molecule differs in relation to other nucleic acid molecules in the plurality as to the Env protein amino acid sequence that it codes for.

9. (withdrawn). A library of Claim 8 wherein the size of the plurality is more than 1 x 10^5.

10. (withdrawn). A cell population comprising a display library of Claims 1, 4, or 8.

11. (withdrawn). A method of creating a viral display library said method comprising the steps of:

(1) randomly integrating nucleotides into viral nucleic acid molecules, the site of said integration in each nucleic acid molecule being within the coding region for an exterior protein of said virus, so as to create a library of viral nucleic acid molecules; and

(2) infecting a population of cells with the nucleic molecules created in step (1) so as to create a library comprising a plurality of viruses wherein for each member of the plurality, the amino acid sequence of the exterior protein coded for by the nucleic acid molecule differs from the amino acid sequence of exterior protein coded for by other members of the plurality, and wherein prior to step (2) each of said nucleic acid molecules further comprises a coding sequence for a cell-selection marker.

12. (withdrawn). A method of Claim 11 wherein the virus is selected from the group consisting of retroviruses, adenoviruses, herpes virus and adeno-associated viruses and alphaviruses.

13. (withdrawn). A method of Claim 12 wherein the virus is a retrovirus and the exterior protein is an Env protein.

14. (withdrawn). A method of Claim 11 wherein the size of the plurality is more than 1×10^5.

15. (presently amended) A method of identifying a retrovirus expressing a feline leukemia virus subgroup A (FeLV-A) or feline leukemia virus subgroup C (FeLV-C) envelope (Env) variant on its surface, said retrovirus capable of transferring its nucleic acid to a host cell, said method comprising the steps of:

(1) infecting ~~administering to~~ a population of host cells[,] with a random display library of retroviruses ~~viruses~~ comprising a plurality of retroviruses ~~viruses~~, wherein each retrovirus ~~virus~~ differs in relation to other retroviruses ~~viruses~~ of the plurality as to an amino acid sequence of a variable region A (VRA) ~~receptor binding domain~~ of an exterior protein, wherein said exterior protein is an envelope (Env) protein[;] , and

~~(2) inoculating said population of host cells with said random display library of viruses to infect said population of host cells with said random display library of viruses,~~ wherein said infecting ~~infection of~~ said host cell population leads to transfer of retroviral nucleic acid to said host cell population; ~~and~~

(2) assaying for retroviral reverse transcriptase in a cell supernatant of said host cell population infected with said random display library of retroviruses, wherein detecting retroviral reverse transcriptase indicates a presence of a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface, wherein expressing said FeLV-A or FeLV-C Env variant on its surface renders said retrovirus capable of infecting a host cell in said host cell population, and

(3) isolating host cell colonies from said host cell population and assaying cell supernatants of isolated host cell colonies for retroviral reverse transcriptase, wherein detection of retroviral reverse transcriptase in a cell supernatant of an isolated host cell colony indicates that said isolated host cell colony is infected with a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface, and thereby identifies ~~identifying~~ a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface ~~that transferred~~ capable of transferring its nucleic acid to ~~one of said~~ a host ~~cells~~ cell.

16. (presently amended) ~~The method of Claim 15~~ A method of identifying a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface, said retrovirus capable of transferring its nucleic acid to a host cell, said method comprising the steps of:

(1) infecting a population of host cells with a random display library of retroviruses comprising a plurality of retroviruses, wherein each retrovirus ~~virus~~ of the plurality comprises a nucleic acid sequence encoding ~~encodes an~~ a FeLV-A or FeLV-C Env variant ~~protein of the virus~~ and a cell-selection marker ~~on the same nucleic acid molecule~~ and ~~wherein step (3) can be achieved by selection~~ each retrovirus differs in relation to other retroviruses of the plurality as to an amino acid sequence of a Variable Region A (VRA) of a FeLV-A or FeLV-C Env protein, wherein said infecting of said host cell population leads to transfer of retroviral nucleic acid to said host cell population;

(2) selecting for retrovirus-infected ~~virus-infected~~ cells expressing the cell-selection marker, wherein expression of said cell-selection marker distinguishes retrovirus-infected cells from uninfected cells in said host cell population; and

(3) isolating said retrovirus-infected cells to identify a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface capable of transferring ~~that transferred~~ its nucleic acid to a ~~said~~ host cell ~~cells~~.

17. (cancelled). A method of Claim 15 wherein the virus is selected from the group consisting of retroviruses, adenoviruses, herpes virus, adeno-associated viruses and alpha viruses.

18. (cancelled).

19. (currently amended) A method of Claim 15 wherein the plurality of retroviruses expressing a FeLV-A or FeLV-C Env variant is more than 1×10^5.

20. (withdrawn). A method of transmitting non-viral nucleic acid to a cell, said

method comprising the steps of:

(1) administering, to a population of host cells, a random display library of viruses, comprising a plurality of viruses wherein each virus differs in relation to other viruses of the plurality as to the amino acid sequence of the exterior protein,

(2) isolating a virus that infected one of said host cells; and

(3) administering the virus isolated in step (2) to a target cell so as to transfer the nonviral nucleic acid to the host cell, wherein prior to step (3) the nonviral nucleic acid sequence intended for delivery to a host cell is incorporated into a nucleic acid viral molecule of said virus.

21. (withdrawn). A method of Claim 20 wherein the nonviral nucleic acid is a gene expressible in said cell.

22. (withdrawn). A method of Claim 20 wherein in step (1) each member of the plurality codes, on the same nucleic acid molecule, for both an exterior protein of the virus and a cell-selection marker and step (2) is achieved by cell selection.

23. (withdrawn). A method of Claim 20 wherein the virus is selected from the group consisting of retroviruses, adenoviruses, herpes virus and adeno-associated viruses and alphaviruses.

24. (withdrawn). A method of Claim 23 wherein the virus is a retrovirus and the exterior protein is an Env protein.

25. (withdrawn). A method of Claim 20 wherein the size of the plurality is more than 1×10^5.

26. (currently amended) A retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface identified using the method of claim 15.

27. (withdrawn). A method for screening a viral display library for variants of a virus that target a known tissue-specific surface protein where the library is expressed on the surface of cells, said virus a library virus, and wherein the tissue-specific surface protein is expressed on the surface of a vector virus, said method comprises the steps of:

(1) administering a vector virus to a population of host cells, said vector virus expressing said tissue-specific protein on its surface, said host cells expressing a random library comprising a plurality of exterior proteins of said library virus, wherein the vector virus being administered comprises a nucleic acid molecule coding for a cell-selection marker and wherein the amino acid sequence of each exterior protein in the plurality differs from the amino acid sequence of other exterior proteins of the plurality; and

(2) isolating a cell that bound to the tissue-specific surface protein on the vector virus being administered or isolating a library virus from said cell.

28. (withdrawn). A method of claim 27 wherein the vector virus administered in step (1) is a pseudotype, such that the tissue-specific surface protein is coded for by a nucleic acid molecule that is not part of the vector virus being administered in step (1).

29. (withdrawn). A method of Claim 27 wherein the library virus is a retrovirus and the exterior protein is an Env protein.

30. (withdrawn). A method of Claim 27 wherein the size of the plurality is more than 1×10^5.

31. (currently amended) A method of identifying a retrovirus expressing a FeLV-A or

FeLV-C Env variant on its surface capable of transferring its nucleic acid to a host cell, said method comprising the steps of:

(1) infecting ~~administering to~~ a population of host cells[,] with a random display library of retroviruses ~~viruses~~ comprising a plurality of retroviruses ~~viruses~~, wherein each retrovirus ~~virus~~ differs in relation to other retroviruses ~~viruses~~ of the plurality as to an amino acid sequence of an exterior protein, wherein said exterior protein is an Env variant ~~protein~~ comprising random amino acid sequences ~~and wherein a divergent amino acid sequence of a receptor binding domain of the Env protein is~~ in ~~the~~ a variable region A (VRA) ~~or variable region B (VRB) of the Env protein~~[;] , and

~~(2) inoculating said population of host cells with said random display library of viruses to infect said population of host cells with said random display library of viruses,~~ wherein said infecting ~~infection~~ of said host cell population leads to transfer of retroviral nucleic acid to said host cell population; ~~and~~

(2) assaying for retroviral reverse transcriptase in a cell supernatant of said host cell population infected with said random display library of retroviruses, wherein detecting retroviral reverse transcriptase indicates a presence of a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface, wherein expressing said FeLV-A or FeLV-C Env variant on its surface renders said retrovirus capable of infecting a host cell in said host cell population, and

(3) isolating host cell colonies from said host cell population and assaying cell supernatants of isolated host cell colonies for retroviral reverse transcriptase, wherein detection of retroviral reverse transcriptase in a cell supernatant of an isolated host cell colony indicates that said isolated host cell colony is infected with a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface, and thereby identifies ~~identifying~~ a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface ~~that transferred~~ capable of transferring its nucleic acid to ~~one of said~~ a host ~~cells~~ cell.

32. (new) The method of Claim 16 wherein the plurality of retroviruses is more than 1 x 10^5.

33. (new) A retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface identified using the method of claim 16.

34. (new) A method of identifying a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface capable of transferring its nucleic acid to a host cell, said method comprising the steps of:

(1) infecting a population of host cells with a random display library of retroviruses comprising a plurality of retroviruses, wherein each retrovirus of the plurality comprises a nucleic acid sequence encoding a FeLV-A or FeLV-C Env variant and a cell-selection marker, and each retrovirus differs in relation to other retroviruses of the plurality as to an amino acid sequence of a FeLV-A or FeLV-C Env protein, said FeLV-A or FeLV-C Env protein comprising random amino acid sequences in a variable region A (VRA);

(2) selecting for retrovirus-infected cells expressing the cell-selection marker, wherein expression of said cell-selection marker distinguishes retrovirus-infected cells from uninfected cells in said host cell population; and

(3) isolating said retrovirus-infected cells to identify a retrovirus expressing a FeLV-A or FeLV-C Env variant on its surface capable of transferring its nucleic acid to a host cell.